

G. E. WOLDT

#5
JRE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/405,940
DATE: 07/10/2000
TIME: 14:51:36

Input Set : A:\09405940.txt
Output Set: N:\CRF3\07102000\I405940.raw

ENTERED

SEQUENCE LISTING

C--> 5 (1) GENERAL INFORMATION:
7 (i) APPLICANT: Hillman, Jennifer L.
8 Corley, Neil C.
C--> 10 (ii) TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
12 (iii) NUMBER OF SEQUENCES: 4
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
16 (B) STREET: 3174 Porter Drive
17 (C) CITY: Palo Alto
18 (D) STATE: CA
19 (E) COUNTRY: USA
20 (F) ZIP: 94304
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Diskette
24 (B) COMPUTER: IBM Compatible
25 (C) OPERATING SYSTEM: DOS
26 (D) SOFTWARE: FastSEQ for Windows Version 2.0
C--> 28 (vi) CURRENT APPLICATION DATA:
C--> 29 (A) APPLICATION NUMBER: US/09/405,940
C--> 30 (B) FILING DATE: 27-Sep-1999
31 (C) CLASSIFICATION:
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: 08/897,097
35 (B) FILING DATE:
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Billings, Lucy J.
39 (B) REGISTRATION NUMBER: 36,749
40 (C) REFERENCE/DOCKET NUMBER: PF-0346 US
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 415-855-0555
44 (B) TELEFAX: 415-845-4166
45 (C) TELEX:
48 (2) INFORMATION FOR SEQ ID NO: 1:
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 314 amino acids
52 (B) TYPE: amino acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
56 (vii) IMMEDIATE SOURCE:
57 (A) LIBRARY: TONGTUT01
58 (B) CLONE: 983910
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
62 Met Gly Thr Arg Leu Leu Cys Trp Ala Ala Leu Cys Leu Leu Gly Ala
63 1 5 10 15
64 Asp His Thr Gly Ala Gly Val Ser Gln Thr Pro Ser Asn Lys Val Thr
65 20 25 30

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66  Glu Lys Gly Lys Asp Val Glu Leu Arg Cys Asp Pro Ile Ser Gly His
67      35      40      45
68  Thr Ala Leu Tyr Trp Tyr Arg Gln Ser Leu Gly Gln Gly Pro Glu Phe
69      50      55      60
70  Leu Ile Tyr Phe Gln Gly Thr Gly Ala Ala Asp Ser Gly Leu Pro
71      65      70      75      80
72  Asn Asp Arg Phe Phe Ala Val Arg Pro Glu Gly Ser Val Ser Thr Leu
73      85      90      95
74  Lys Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Ala Tyr Leu Arg Ala
75      100     105     110
76  Gly Val Ala Ala Gly Trp Ser Ser Tyr Asn Glu Gln Tyr Phe Gly Pro
77      115     120     125
78  Gly Thr Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro
79      130     135     140
80  Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln
81      145     150     155     160
82  Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val
83      165     170     175
84  Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
85      180     185     190
86  Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg
87      195     200     205
88  Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn
89      210     215     220
90  Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu
91      225     230     235     240
92  Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val
93      245     250     255
94  Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser
95      260     265     270
96  Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu
97      275     280     285
98  Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met
99      290     295     300
100 Ala Met Val Lys Arg Lys Asp Ser Arg Gly
101      305     310
103 (2) INFORMATION FOR SEQ ID NO: 2:
105   (i) SEQUENCE CHARACTERISTICS:
106       (A) LENGTH: 1200 base pairs
107       (B) TYPE: nucleic acid
108       (C) STRANDEDNESS: single
109       (D) TOPOLOGY: linear
111   (vii) IMMEDIATE SOURCE:
112       (A) LIBRARY: TONGTUT01
113       (B) CLONE: 983910
115   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
117 GTAAAGCTCC CATCCTGCCC TGA CTCTGTC ATGGGCACCA GGCTCCTCTG CTGGGCAGCC      60
118 CTGTGCCCTCC TGGGGGCAGA TCACACAGGT GCTGGAGTCT CCCAGACCCC CAGTAACAAG      120
119 GTCACAGAGA AGGGAAGA TGTAGAGCTC AGGTGTGATC CAATTTCAGG TCATACTGCC      180

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120 CTTTACTGGT ACCGACAAAG CCTGGGGCAG GCCCAGAGT TTCTAATTTA CTCCAAGGC 240
121 ACGGGTGCGG CAGATGACTC AGGGCTGCCC AACGATCGGT TCTTTGCAGT CAGGCCTGAG 300
122 GGATCCGTCT CTACTCTGAA GATCCAGCGC ACAGAGCAGG GGGACTCAGC CGCGTATCTC 360
123 CGTGCCGGCG TTGCGGCGGG ATGGAGCTCC TACAATGAGC AGTATTTTGG CCCAGGCACC 420
124 CGGCTGACAG TGCTAGAGGA CCTGAAAAAC GTGTTCCAC CCAGGTCGC TGTGTTTGAG 480
125 CCATCAGAAG CAGAGATCTC CCACACCCAA AAGGCCACAC TGGTGTGCCT GGCCACAGGC 540
126 TTCTACCCCG ACCACGTGGA GCTGAGCTGG TGGGTGAATG GGAAGGAGGT GCACAGTGGG 600
127 GTCAGCACAG ACCCGCAGCC CCTCAAGGAG CAGCCCGCCC TCAATGACTC CAGATACTGC 660
128 CTGAGCAGCC GCCTGAGGGT CTCGGCCACC TTCTGGCAGA ACCCCCGCAA CCACTTCCGC 720
129 TGTCAAGTCC AGTTCTACGG GCTCTCGGAG AATGACGAGT GGACCCAGGA TAGGGCCAAA 780
130 CCTGTCAACC AGATCGTCAG CGCCGAGGCC TGGGGTAGAG CAGACTGTGG CTTACCTCC 840
131 GAGTCTTACC AGCAAGGGGT CCTGTCTGCC ACCATCCTCT ATGAGATCTT GCTAGGGAAG 900
132 GCCACCTTGT ATGCCGTGCT GGTCAAGTGC CTCGTGCTGA TGGCCATGGT CAAGAGAAAG 960
133 GATTCCAGAG GCTAGCTCCA AAACCATCCC AGGTCATTCT TCATCCTCAC CCAGGATTCT 1020
134 CCTGTACCTG CTCCCAATCT GTGTTCTTAA AAGTGATTCT CACTCTGCTT CTCATCTCCT 1080
135 ACTTACATGA ATACTTCTCT CTTTTTCTG TTCCCTGAA GATTGAGCTC CCAACCCCA 1140
136 AGTACGAAAT AGGCTAAACC AATAAAAAAT TGTGTGTTGG GCCTGGTTGC AAAAAAATA 1200
138 (2) INFORMATION FOR SEQ ID NO: 3:
140 (i) SEQUENCE CHARACTERISTICS:
141 (A) LENGTH: 311 amino acids
142 (B) TYPE: amino acid
143 (C) STRANDEDNESS: single
144 (D) TOPOLOGY: linear
146 (vii) IMMEDIATE SOURCE:
147 (A) LIBRARY: GenBank
148 (B) CLONE: 1100182
150 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
152 Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
153 1 5 10 15
154 Asp His Ala Asp Thr Gly Val Ser Gln Asn Pro Arg His Lys Ile Thr
155 20 25 30
156 Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
157 35 40 45
158 Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
159 50 55 60
160 Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
161 65 70 75 80
162 Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
163 85 90 95
164 Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
165 100 105 110
166 Ser Ser Pro Gly Thr Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg
167 115 120 125
168 Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala
169 130 135 140
170 Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
171 145 150 155 160
172 Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
173 165 170 175

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```

174 Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro
175      180      185      190
176 Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
177      195      200      205
178 Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
179      210      215      220
180 His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
181      225      230      235      240
182 Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
183      245      250      255
184 Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
185      260      265      270
186 Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala
187      275      280      285
188 Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val
189      290      295      300
190 Lys Arg Lys Asp Ser Arg Gly
191      305      310
193 (2) INFORMATION FOR SEQ ID NO: 4:
195   (i) SEQUENCE CHARACTERISTICS:
196       (A) LENGTH: 310 amino acids
197       (B) TYPE: amino acid
198       (C) STRANDEDNESS: single
199       (D) TOPOLOGY: linear
201   (vii) IMMEDIATE SOURCE:
202       (A) LIBRARY: GenBank
203       (B) CLONE: 339012
205   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
207 Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
208   1      5      10      15
209 Asp His Ala Asp Thr Gly Val Ser Gln Asn Pro Arg His Asn Ile Thr
210      20      25      30
211 Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
212      35      40      45
213 Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
214      50      55      60
215 Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
216      65      70      75      80
217 Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
218      85      90      95
219 Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
220      100     105     110
221 Ser Ser Leu Ala Gly Leu Asn Gln Pro Gln His Phe Gly Asp Gly Thr
222      115     120     125
223 Arg Leu Ser Ile Leu Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val
224      130     135     140
225 Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala
226      145     150     155     160
227 Thr Leu Val Cys Leu Ala Thr Gly Ile Phe Pro Asp His Val Glu Leu

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```

228                               165                               170                               175
229 Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
230                               180                               185                               190
231 Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys
232                               195                               200                               205
233 Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg
234                               210                               215                               220
235 Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp
236 225                               230                               235                               240
237 Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala
238                               245                               250                               255
239 Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln
240                               260                               265                               270
241 Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys
242                               275                               280                               285
243 Ala Thr Met Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met
244                               290                               295                               300
245 Val Lys Arg Lys Asp Phe
246 305                               310

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VERIFICATION SUMMARY DATE: 07/10/2000
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Input Set : A:\09405940.txt
Output Set: N:\CRF3\07102000\I405940.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:10 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:28 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]